

# Package ‘DMRcatedata’

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**Type** Package

**Title** Data Package for DMRcate

**Version** 2.31.0

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**Author** Tim Peters

**Maintainer** Tim Peters <t.peters@garvan.org.au>

**Description** This package contains 9 data objects supporting functionality and examples of the Bioconductor package DMRcate.

**License** GPL-3

**Depends** R (>= 4.0), ExperimentHub

**Imports** GenomicFeatures, Gviz, readxl, plyr, rtracklayer,  
IlluminaHumanMethylation450kanno.ilmn12.hg19,  
IlluminaHumanMethylationEPICanno.ilm10b4.hg19

**LazyData** true

**Suggests** knitr

**biocViews** ExperimentHub, ExperimentData, SNPData, Homo\_sapiens\_Data,  
Mus\_musculus\_Data, SequencingData, MicroarrayData, Genome

**VignetteBuilder** knitr

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|                     |   |
|---------------------|---|
| DMRcatedata-package | <i>Dataset to use with the DMRcate pipeline</i> |
|---------------------|---|

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### Description

SNP annotation, cross-hybridising probes, XY probes, and gene annotation for hg19, hg38 and mm10

### Author(s)

Tim Peters, Immunogenomics Laboratory, Garvan Institute of Medical Research  
 Maintainer: Tim Peters<t.peters@garvan.org.au>

### Examples

```
data(crosshyb)
data(snpsall)
data(hg19.grt)
data(hg19.generanges)
```

---

|          |   |
|----------|---|
| ALLbetas | <i>EPICv2 beta values for DMR calling</i> |
|----------|---|

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### Description

Matrix of EPICv2 beta values from Noguera-Castells et al. (2023) consisting of five B cell acute lymphoblastic leukaemia (BALL) and five T cell acute lymphoblastic leukaemia (TALL) samples for DMR calling.

### Usage

```
data(ALLbetas)
```

### Format

```
data.frame
```

### Source

[https://ftp.ncbi.nlm.nih.gov/geo/series/GSE222nnn/GSE222919/suppl/GSE222919\\_processed\\_data.txt.gz](https://ftp.ncbi.nlm.nih.gov/geo/series/GSE222nnn/GSE222919/suppl/GSE222919_processed_data.txt.gz)

---

`crosshyb`*Potentially cross-hybridising Illumina probes*

---

**Description**

This is a character vector of Illumina probes whose probe sequence promiscuously aligns to non-target sections of the genome with a matching of 47bp or higher.

**Usage**

```
data(crosshyb)
```

**Format**

character

**Source**

[https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM2\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM2_ESM.csv) (accessed September 2019) [https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM3\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM3_ESM.csv) (accessed September 2019) <http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48639-non-specific-probes-Illumina450k.xlsx> (accessed September 2019)

---

`epicv2snps`*SNP information for EPICv2 Illumina probes*

---

**Description**

This is a data.frame of Illumina probes from EPICv2 whose target CpG lies on or near a known SNP. SNP ID, distance and minor allele frequency are all reported here.

**Usage**

```
data(snpsall)
```

**Format**

data.frame

**Source**

[https://static-content.springer.com/esm/art%3A10.1186%2Fs12864-024-10027-5/MediaObjects/12864\\_2024\\_10027\\_MOESM4\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs12864-024-10027-5/MediaObjects/12864_2024_10027_MOESM4_ESM.csv)

---

|                 |  |
|-----------------|--|
| hg19.generanges | <i>Start and stop positions of all genes in hg19</i> |
|-----------------|--|

---

**Description**

This data set gives the genomic intervals of all gene regions in the Ensembl Release 75 of hg19.

**Usage**

```
data(hg19.generanges)
```

**Format**

A GRanges object with 57773 intervals.

**Source**

```
ftp://ftp.ensembl.org/pub/release-75/gtf/homo_sapiens/Homo_sapiens.GRCh37.75.gtf.gz
```

---

|          |                                 |
|----------|---------------------------------|
| hg19.grt | <i>GeneRegionTrack for hg19</i> |
|----------|---------------------------------|

---

**Description**

This is a GeneRegionTrack formulated from TxDb.Hsapiens.UCSC.hg19.knownGene.

**Usage**

```
data(hg19.grt)
```

**Format**

GeneRegionTrack

---

|                 |  |
|-----------------|--|
| hg38.generanges | <i>Start and stop positions of all genes in hg38</i> |
|-----------------|--|

---

**Description**

This data set gives the genomic intervals of all gene regions in the Ensembl Release 102 of hg38.

**Usage**

```
data(hg38.generanges)
```

**Format**

A GRanges object with 60616 intervals.

**Source**

[ftp://ftp.ensembl.org/pub/release-102/gtf/homo\\_sapiens/Homo\\_sapiens.GRCh38.102.chr.gtf.gz](ftp://ftp.ensembl.org/pub/release-102/gtf/homo_sapiens/Homo_sapiens.GRCh38.102.chr.gtf.gz)

---

|          |                                 |
|----------|---------------------------------|
| hg38.grt | <i>GeneRegionTrack for hg38</i> |
|----------|---------------------------------|

---

**Description**

This is a GeneRegionTrack formulated from TxDb.Hsapiens.UCSC.hg38.knownGene.

**Usage**

```
data(hg38.grt)
```

**Format**

GeneRegionTrack

mm10.generanges      *Start and stop positions of all genes in mm10*

---

**Description**

This data set gives the genomic intervals of all gene regions in the Ensembl Release 102 of mm10.

**Usage**

```
data(mm10.generanges)
```

**Format**

A GRanges object with 55401 intervals.

**Source**

[ftp://ftp.ensembl.org/pub/release-96/gtf/mus\\_musculus/Mus\\_musculus.GRCm38.102.chr.gtf.gz](ftp://ftp.ensembl.org/pub/release-96/gtf/mus_musculus/Mus_musculus.GRCm38.102.chr.gtf.gz)

---

mm10.grt      *GeneRegionTrack for mm10*

---

**Description**

This is a GeneRegionTrack formulated from TxDb.Mmusculus.UCSC.mm10.knownGene.

**Usage**

```
data(mm10.grt)
```

**Format**

GeneRegionTrack

---

`snpsall`*SNP information for EPICv1 and 450K Illumina probes*

---

**Description**

This is a data.frame of Illumina probes from EPICv1 and 450K whose target CpG lies on or near a known SNP. SNP ID, distance and minor allele frequency are all reported here.

**Usage**

```
data(snpsall)
```

**Format**

```
data.frame
```

**Source**

[https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM4\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM4_ESM.csv) (accessed September 2019) [https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM5\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM5_ESM.csv) (accessed September 2019) [https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059\\_2016\\_1066\\_MOESM6\\_ESM.csv](https://static-content.springer.com/esm/art%3A10.1186%2Fs13059-016-1066-1/MediaObjects/13059_2016_1066_MOESM6_ESM.csv) (accessed September 2019) <http://www.sickkids.ca/MS-Office-Files/Research/WeksbergLab/48640-polymorphic-CpGs-Illumina.xlsx> (accessed September 2019)

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`XY.probes`*Sex chromosome Illumina probes*

---

**Description**

This is a character vector of Illumina probes whose target CpG site is on a sex chromosome.

**Usage**

```
data(XY.probes)
```

**Format**

```
character
```

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